Supplementary Figure 1 Multiple sequence alignment of LAR and IFR proteins as well as distantly related ANR and DFR proteins of the Reductase-Epimerase-Dehydratase superfamily that is the basis of the phylogenetic tree of Figure 2. The alignment was formed by the ClustalW program using the default parameters of the MEGA program (Kumar et al., 2004). Residues highlighted in black and gray are conserved in all proteins in the alignment. The residues highlighted in yellow are the RFLP, ICCN and THD motifs conserved in the LAR sequences but not conserved in the related IFR subfamily and more distant RED homologues. The alignemnt includes all related proteins from the Arabidopsis genome (designated according to their AGI number) to give an indication of how the proteins from other species fit into a complete genome. Also included are enzymes for which a catalytic function has been shown such as IFR, PLR , PCBER in the IFR sub-family, Arabidopsis and Medicago ANR and Arabidopsis and maize DFR. The IFR sub-family includes six grape IFR-like (IFRL) proteins found in the grape EST collections (IFRL_Vitvi1-6, BN000706-11). The ANR/DFR group shows only a small fraction of the proteins in this branch of the RED superfamily. The Arabidopsis proteins most closely related to ANR (At4g27250) and DFR (At2g45400) are also included. The proteins are labeled according to their proposed catalytic activity followed by the species they come from, e.g. LAR_ Desun is LAR from *Desmodium uncinatum* (Q84V83). Other species represented in the phylogenetic tree and database accession numbers are *Cicer arietinum* (IFR, Q00016), *Forsythia x intermedia* (PLR, AAC49608; PCBER, AAF64174), *Gossypium arboretum* (ANR CAD91910; LAR1, BN000695; LAR2, BN000699), *Gossypium raimondii* (LAR1, BN000700; LAR2, BN000701), *Hordeum vulgare* (LAR, BN000696), *Medicago truncatula* (ANR, AAN77735; LAR, BN000703), *Oryza sativa* (LAR, BN000704), *Phaseolus coccineus* (ANR, CAD91909; LAR, BN000698), *Pinus taeda* (LAR, BN000697), *Vitis shuttleworthii* (LAR1, BN000702), *Vitis vinifera* (ANR, CAD91911; DFR, P51110; LAR1, AJ865336; LAR2, AJ865334), and *Zea mays* (DFR, CAA28734).

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                      *        20         *        40         *        60         *
LAR Orysa  : --------------------------------------MAPAAQELLLQEVPQPRRTGAALIVGATGYIGRFVAE :  37
LAR Desun  : -------------------------------------------MTVS--GAIPSMTKNRTLVVGGTGFIGQFITK :  30
LAR1 Pinta : MACATDVARQFLPCVQPVPSSMGGETARSINLTCNGLSPPQPQYNAENNHDQDTTVATRVLIIGATGFIGRFVAE :  75
LAR1 Vitvi : -----------------------------------------------MTVSPVPSPKGRVLIAGATGFIGQFVAT :  28
LAR2 Vitvi : -------------------------------------MTVLSVSTPPAPQAPPAATGPRTLVVGASGFIGRFVAE :  38
LAR1 Vitsh : -----------------------------------------------MTVSPVPSLKGRVLIAGATGFIGQFVAA :  28
LAR Horvu  : --------------------------------------MAPC--EELQEEVA---RSGPALIVGATGYIGRFVAE :  32
LAR Medtr  : -------------------------------------------MAPSSSPTTP-ISKGRVLIVGATGFMGKFVTE :  31
LAR Phaco  : -------------------------------------------MVTS--PTIPSHTKARVLIIGATGFIGKFVTE :  30
LAR2 Gosar : -----------------------------------------MKSTQMNGSYPNESEAGQTVVIGSSGFIGRFITE :  34
LAR2 Gosra : -----------------------------------------MKSTHMNGSYPNESETGQTLVIGSSGFIGRFITE :  34
LAR1 Gosar : -----------------------------------------------MTVS---VANGRVLIVGATGFIGRFVAD :  25
LAR1 Gosra : -----------------------------------------------MTVS---VANGRVLIVGATGFIGRFVAD :  25
IFRL1 Vitv : ------------------------------------------------------MEKSKVLVVGGTGYIGRRMVE :  21
IFRL2 Vitv : ---------------------------------------------QQSSGKAMESVLSIILIFGGTGYIGRYMVK :  30
IFRL3 Vitv : ----------------------------------------------------MVCEKSKILVFGATGYLGKYMVK :  23
IFRL4 Vitv : -----------------------------------------------------MAEKSKILIIGGTGYIGKFVVQ :  22
IFRL5 Vitv : -----------------------------------------------------MSEKSKILIIGGTGYIGKFIVA :  22
IFRL6 Vitv : -----------------------------------------------------MSDKSKILIIGGTGYIGKFIVA :  22
At1g19540  : -------------------------------------------------------MTSKILVIGATGLIGKVLVE :  20
At1g32100  : ------------------------------------------------MGESKRTEKTRVLVVGATGYIGKRIVR :  27
At1g75280  : ----------------------------------------------------MATEKSKILVIGGTGYIGKFLVE :  23
At1g75290  : ----------------------------------------------------MASEKSKILVIGGTGHIGKLIIE :  23
At1g75300  : ----------------------------------------------------MTTEKSKILVIGGTGYMGEFIVE :  23
At4g13660  : ------------------------------------------------MKETNFGEKTRVLVVGGTGSLGRRIVS :  27
At4g34540  : --------------------------------------------------MEEEKKKSRVLIIGATGRLGNYLTR :  25
At4g39230  : -----------------------------------------------------MTSKSKILFIGGTGYIGKYIVE :  22
PLR Forin  : ------------------------------------------------------MGKSKVLIIGGTGYLGRRLVK :  21
PCBER Fori : -----------------------------------------------------MAEKTKILIIGGTGYIGKFVAE :  22
IFR Cicar  : -----------------------------------------------------MASQNRILVLGPTGAIGRHVVW :  22
DFR At5g42 : ----------------------------------------------------MVSQKETVCVTGASGFIGSWLVM :  23
At2g45400  : --------------------MVREEQEEDDNNNNNNGGGERKLLVADETVPSLLDETGLVCVTGGSGFVASWLIM :  55
DFR Vitvi  : ----------------------------------------------------MGSQSETVCVTGASGFIGSWLVM :  23
DFR MAIZE  : -----------------------------------------------MERGAGASEKGTVLVTGASGFVGSWLVM :  28
At4g27250  : -----------------------------------------------MELQGEESKTATYCVTGASGYIGSWLVK :  28
ANR Medtr  : ----------------------------------------------MASIKQIEIEKKKACVIGGTGFVASLLIK :  29
ANR Arath  : ---------------------------------------------MDQTLTHTG--SKKACVIGGTGNLASILIK :  28
ANR Phaco  : ----------------------------------------------MATVKKIG---KKACVIGGSGFMASCLVK :  26
ANR Gosar  : ----------------------------------------------MASQL-VG--TKRACVVGGSGFVASLLVK :  26
ANR_Vitvi  : ----------------------------------------------MATQHPIG--KKTACVVGGTGFVASLLVK :  27
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                80         *       100         *       120         *       140         *
LAR Orysa  : ACLDSGRDTFILVRPG----------NACP--ARAASVDALRQKGAVVIEGCVGGKEGRKSVEAALRARGVEVVI : 100
LAR Desun  : ASLGFGYPTFLLVRPG----------PVSP--SKAVIIKTFQDKGAKVIYGVINDKE---CMEKILKEYEIDVVI :  90
LAR1 Pinta : ASVKSGRPTYALVRPT----------TLSS---KPKVIQSLVDSGIQVVYGCLHDHN---SLVKAIR--QVDVVI : 132
LAR1 Vitvi : ASLDAHRPTYILARPG----------PRSP--SKAKIFKALEDKGAIIVYGLINEQE---AMEKILKEHEIDIVV :  88
LAR2 Vitvi : ASLSPGHPTYVLVRSS----------ATTSS-SKASTIKSLEDQGAILVTGSIGDKE---VMIEILRKYEIEVVI :  99
LAR1 Vitsh : ASLDAHRPTYILARPG----------PRSP--SKAKIIKAHEDKGAIIVYGLINEQE---SMEKILKEHEIDIVV :  88
LAR Horvu  : ACLDSGRRTFILVRPG----------NACP--ARAASVDALLRKGAFVVEGRVDGKDGKRSVETALRAHGIEVVI :  95
LAR Medtr  : ASISTAHPTYLLIRPG----------PLIS--SKAATIKTFQEKGAIVIYGVVNNKE---FVEMILKKYEIDTVI :  91
LAR Phaco  : ASLLTAHPTYLLLRPP----------PLVP--SKDAIVKTFQEKGAMIIHGVINNKD---FVEKILKEHEIDIVI :  90
LAR2 Gosar : ACLDSGRPTYILVRSS----------SN-SP-SKASTIKFLQDKGAIVIYGSITDQE---FMEKVLREYKIEVVI :  94
LAR2 Gosra : ACLDSGRPTYILVRSS----------SN-SP-SKASTIKFLQDKGAIVIYGSITDQE---FMEKVLREYKIEVVI :  94
LAR1 Gosar : ASLDAGRPTYVLVRPS----------SGNQY-SKDKVAKALQDRGAILLNGLANDKE---LMVKLLKEHQIEIVI :  86
LAR1 Gosra : ASLDAGRPTYVLVRPS----------SGNQY-SKDKVAKALRDRGAILLNGLANDKE---LMVKLLKEHQIEIVI :  86
IFRL1 Vitv : ASLAQGHPTFVLQRPE-----------IGMDIEKLQMLLSFKAKGATLVEGSFADHK-----SLVEAVKKVDVVI :  80
IFRL2 Vitv : ASVKMGHPTYVYSRPM----------TPQTHPSKIELLKEFQSMGVNIVQGELDEHEK-----LVSVIQQVDVVI :  90
IFRL3 Vitv : ASVSMGHPTYAYVRPA----------NPDAKPSKLPQHRELESLGVTIFQGELDEHET-----MVAALKQVDVVI :  83
IFRL4 Vitv : ASAKSGHPTFALVRES-----------TIADPVKGKLIQEFKNSGVTLLHGDLYDHD-----SLVKAIKQVDVVI :  81
IFRL5 Vitv : ASAKSGHPTFALVRES-----------TVS--EKFEIIESFKSSGVTLVYGDLYDHE-----SLVKAIKQVDVVI :  79
IFRL6 Vitv : ASARLGHPTFALIRES-----------TVSNPSKSGIIESFKSSGVSLVYGDLYDHE-----SLVKAIKQVDVVI :  81
At1g19540  : ESAKSGHATFALVREA-----------SLSDPVKAQLVERFKDLGVTILYGSLSDKE-----SLVKAIKQVDVVI :  79
At1g32100  : ACLAEGHETYVLQRPE-----------IGLEIEKVQLFLSFKKLGARIVEGSFSDHQ-----SLVSAVKLVDVVV :  86
At1g75280  : ASAKAGHSTFALVREA-----------TLSDPVKGKTVQSFKDLGVTILHGDLNDHE-----SLVKAIKQVDVVI :  82
At1g75290  : ASVKAGHSTLALVREA-----------SLSDPNKGKTVQNFKDFGVTLLHGDLNDHE-----SLVKAIKQADVVI :  82
At1g75300  : GSAKAGNPTFALVREA-----------SLSDPVKSKTIQSFKDLGVTILHGDLNDHE-----SLVKAIKQVDVVI :  82
At4g13660  : ACLAEGHETYVLQRPE-----------IGVDIEKVQLLLSFKRLGAHLVEGSFSDHQ-----SLVSAVKQVDVVV :  86
At4g34540  : FSIESGHPTFALIRNT----------------TLSDKLKSLSDAGVTLLKGSLEDEG-----SLAEAVSKVDVVI :  79
At4g39230  : ASARSGHPTLVLVRNS-----------TLTSPSRSSTIENFKNLGVQFLLGDLDDHT-----SLVNSIKQADVVI :  81
PLR Forin  : ASLAQGHETYILHRPE-----------IGVDIDKVEMLISFKMQGAHLVSGSFKDFN-----SLVEAVKLVDVVI :  80
PCBER Fori : ASAKSGHPTFALFRES-----------TISDPVKGKIIEGFKNSGVTILTGDLYDHE-----SLVKAIKQVDVVI :  81
IFR Cicar  : ASIKAGNPTYALIRKTPGDINKPSLVAAANPESKEELLQSFKAAGVILLEGDMNDHE-----ALVKAIKQVDTVI :  92
DFR At5g42 : RLLERGYFVRATVRD-------------PGNLKKVQHLLDLPNAKTLLTLWKADLSEEGSYDDAINGCDGVFHVA :  85
At2g45400  : RLLQRGYSVRATVRTN-----------SEGNKKDISYLTELPFASERLQIFTADLNEPESFKPAIEGCKAVFHVA : 119
DFR Vitvi  : RLLERRLTVRATVRD-------------PTNVKKVKHLLDLPKAETHLTLWKADLADEGSFDEAIKGCTGVFHVA :  85
DFR MAIZE  : KLLQAGYTVRATVRD-------------PANVGKTKPLMDLPGATERLSIWKADLAEEGSFHDAIRGCTGVFHVA :  90
At4g27250  : SLLQRGYTVHATLRD----------------LAKSEYFQSKWKENERLRLFRADLRDDGSFDDAVKGCDGVFHVA :  87
ANR Medtr  : QLLEKGYAVNTTVRD-------------LDSANKTSHLIALQSLGE-LNLFKAELTIEEDFDAPISGCELVFQLA :  90
ANR Arath  : HLLQSGYKVNTTVRD-------------PENEKKIAHLRKLQELGD-LKIFKADLTDEDSFESSFSGCEYIFHVA :  89
ANR Phaco  : QLLHKGYAVNTTVRD-------------PDNAKKISHLLALQSLGD-LNIFGADLTGERDFDAPIAGCELVFQLA :  87
ANR Gosar  : LLLEKGFAVNTTVRD-------------PDNQKKISHLVTLQELGD-LKIFQADLTDEGSFDAPIAGCDLVFHVA :  87
ANR_Vitvi  : LLLQKGYAVNTTVRD-------------PDNQKKVSHLLELQELGD-LKIFRADLTDELSFEAPIAGCDFVFHVA :  88
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                     160        *       180         *       200         *       220
LAR Orysa  : SVMG-------------------GASILDQLGLIEAIRAAGTVKRFLPS--EFGHDVDR--ARPVGAGLRFYEEK : 152
LAR Desun  : SLVG-------------------GARLLDQLTLLEAIKSVKTIKRFLPS--EFGHDVDR--TDPVEPGLTMYKEK : 142
LAR1 Pinta : STVG-------------------GALILDQLKIVDAIKEVGTVKRFLPS--EFGHDVDR--ADPVEPALSFYIEK : 184
LAR1 Vitvi : STVG-------------------GESILDQIALVKAMKAVGTIKRFLPS--EFGHDVNR--ADPVEPGLNMYREK : 140
LAR2 Vitvi : SAVG-------------------GATILDQLTLAEAIKAVGSIKRFLPS--EFGHDIDR--AEPVEPGLTMYMEK : 151
LAR1 Vitsh : STVG-------------------GESILDQIALVKAMKAVGTIKRFLPS--EFGHDVNR--ADPVEPGLNMYREK : 140
LAR Horvu  : SVMG-------------------GANILDQLGLIKAIQAAGTVKRFLPS--EFGHDVDR--ARPVGAGLGFYEEK : 147
LAR Medtr  : SAIG-------------------AESLLDQLTLVEAMKSIKTIKRFLPS--EFGHDVDR--ADPVEPGLAMYKQK : 143
LAR Phaco  : SAIG-------------------AKSLLDQLILVEAMKSLKTIKRFLAS--KFGHDVDR--ADPVEPGLTMYKEK : 142
LAR2 Gosar : SAVG-------------------GESILDQLSLIEAIKNVNTVKRFVPS--EFGHDIDR--AEPVEPGLTMYEQK : 146
LAR2 Gosra : SAVG-------------------GESILDQFSLIEAIKNVNTVKRFVPS--EFGHDIDR--AEPVEPGLTMYEQK : 146
LAR1 Gosar : SALG-------------------GATILDQLSLVEAIHSVGTVKRFLPS--EFGHDVDR--ADPVEPGLTMYKEK : 138
LAR1 Gosra : SALG-------------------GATILDQLSLVEAIHSAGTVKRFLPS--EFGHDVDR--ADPVEPGLTMYKEK : 138
IFRL1 Vitv : CTMSGV--------------HFRSHNLLMQLKLVEAIKEAGNIKRFLPS--EFGMDPAR-MEDALEPGRVTFDEK : 138
IFRL2 Vitv : SALA-------------------YPQVLDQLKIIDAIKVAGTTKRFLPS--DFGVEEDS--VTVLSPFQDFLDKK : 142
IFRL3 Vitv : STLA-------------------VPQHLEQFKIIDAIKKAGNIKEGLSHR-SFGNEVDR--VSGLPPFQALLENK : 136
IFRL4 Vitv : STVG-------------------FMQLADQVKIIAAIKEAGNVKRFLPS--EFGNDVDR--VNAVEPAKSAFAAK : 133
IFRL5 Vitv : STVG-------------------HAQLPDQVKIIAAIKEAGNVKRFFPS--EFGNDVDR--VHAVEPAKTAFATK : 131
IFRL6 Vitv : STVG-------------------RAQLSDQVKIIAAIKEAGNVKRFFPS--EFGNDVDR--VHAVGPAKTAFEIK : 133
At1g19540  : SAVGRF-----------------QTEILNQTNIIDAIKESGNVKRFLPS--EFGNDVDR--TVAIEPTLSEFITK : 133
At1g32100  : SAMSGV--------------HFRSHNILVQLKLVEAIKEAGNVKRFLPS--EFGMDPPR-MGHALPPGRETFDQK : 144
At1g75280  : STVG-------------------SMQILDQTKIISAIKEAGNVKRFLPS--EFGVDVDR--TSAVEPAKSAFAGK : 134
At1g75290  : STVG-------------------SMQILDQTKIISAIKEAGNVKRFLPS--EFGMDVDK--SSAVEPAKSAFGRK : 134
At1g75300  : STIG-------------------HKQIFDQTKIISAIKEAGNVKRFLPA--EFGIDVER--TSAVEPAKSLFAGK : 134
At4g13660  : SAMSGV--------------HFRTHNIPVQLKLVAAIKEAGNVKRFLPS--EFGMDPSR-MGHAMPPGSETFDQK : 144
At4g34540  : SAIP-------------------SKHVLDQKLLVRVIKQAGSIKRFIPA--EYGANPDK--TQVSDLDHDFYSKK : 131
At4g39230  : STVG-------------------HSLLGHQYKIISAIKEAGNVKRFFPS--EFGNDVDR--VFTVEPAKSAYATK : 133
PLR Forin  : SAISGV--------------HIRSHQILLQLKLVEAIKEAGNVKRFLPS--EFGMDPAKFMDTAMEPGKVTLDEK : 139
PCBER Fori : STVG-------------------SLQLADQVKIIAAIKEAGNVKRFFPS--EFGTDVDR--CHAVEPAKSSYEIK : 133
IFR Cicar  : CTFG-------------------RLLILDQVKIIKAIKEAGNVKRFFPS--EFGLDVDR--HDAVDPVRPVFDEK : 144
DFR At5g42 : TPMDFESKDP--------ENEVIKPTVNGMLGIMKACVKAKTVRRFVFTSSAGTVNVEEHQKN---VYDENDWSD : 149
At2g45400  : HPMDPNSNET--------EETVTKRTVQGLMGILKSCLDAKTVKRFFYTSSAVTVFYSGGNGGGGGEVDESVWSD : 186
DFR Vitvi  : TPMDFESKDP--------ENEVIKPTIEGMLGIMKSCAAAKTVRRLVFTSSAGTVNIQEHQLP---VYDESCWSD : 149
DFR MAIZE  : TPMDFLSKDP--------ENEVIKPTVEGMISIMRACKEAGTVRRIVFTSSAGTVNLEERQRP---VYDEESWTD : 154
At4g27250  : ASMEFDISSDHVNLESYVQSKVIEPALKGVRNVLSSCLKSKSVKRVVFTSSISTLTAKDENERMRSFVDETCKAH : 162
ANR Medtr  : TPVNFASQDP--------ENDMIKPAIKGVLNVLKACVRAKEVKRVILTSSAAAVTINELEGTG-HVMDETNWSD : 156
ANR Arath  : TPINFKSEDP--------EKDMIKPAIQGVINVLKSCLKSKSVKRVIYTSSAAAVSINNLSGTG-IVMNEENWTD : 155
ANR Phaco  : TPVNFASEDP--------ENDMIKPAISGVLNVLKACARVKGVKRVILTSSAAAVTINPVKDTG-LVMDESNWTD : 153
ANR Gosar  : TPVNFASEDP--------ENDMIKPATQGVVNVLKACAKAKTVKRVVLTSSAAAVSINTLDGTD-LVMTEKDWTD : 153
ANR_Vitvi  : TPVHFASEDP--------ENDMIKPAIQGVVNVMKACTRAKSVKRVILTSSAAAVTINQLDGTG-LVVDEKNWTD : 154
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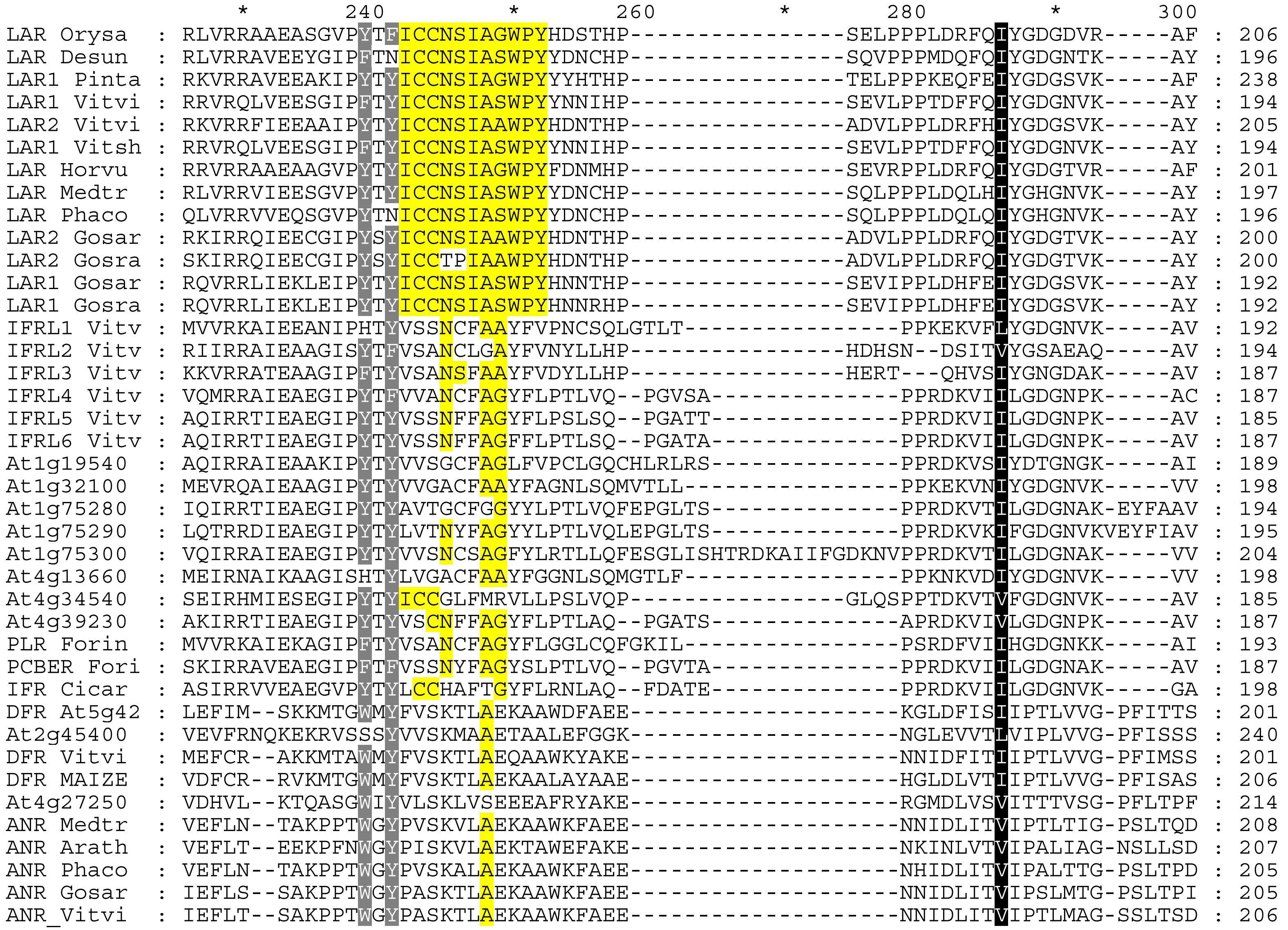

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                  *       240         *       260         *       280         *       300
LAR Orysa   : RLVRRAAEASGVPYTFICCNSIAGWPYHDSTHP----------------SELPPPLDRFQIYGDGDVR-----AF : 206
LAR Desun   : RLVRRAVEEYGIPFTNICCNSIASWPYYDNCHP----------------SQVPPPMDQFQIYGDGNTK-----AY : 196
LAR1 Pinta  : RKVRRAVEEAKIPYTYICCNSIAGWPYYYHTHP----------------TELPPPKEQFEIYGDGSVK-----AF : 238
LAR1 Vitvi  : RRVRQLVEESGIPFTYICCNSIASWPYYNNIHP----------------SEVLPPTDFFQIYGDGNVK-----AY : 194
LAR2 Vitvi  : RKVRRFIEEAAIPYTYICCNSIAAWPYHDNTHP----------------ADVLPPLDRFHIYGDGSVK-----AY : 205
LAR1 Vitsh  : RRVRQLVEESGIPFTYICCNSIASWPYYNNIHP----------------SEVLPPTDFFQIYGDGNVK-----AY : 194
LAR Horvu   : RRVRRAAEAAGVPYTYICCNSIAGWPYFDNMHP----------------SEVRPPLDRFQIYGDGTVR-----AF : 201
LAR Medtr   : RLVRRVIEESGVPYTYICCNSIASWPYYDNCHP----------------SQLPPPLDQLHIYGHGNVK-----AY : 197
LAR Phaco   : QLVRRVVEQSGVPYTNICCNSIASWPYYDNCHP----------------SQLPPPLDQLQIYGHGNVK-----AY : 196
LAR2 Gosar  : RKIRRQIEECGIPYSYICCNSIAAWPYHDNTHP----------------ADVLPPLDRFQIYGDGTVK-----AY : 200
LAR2 Gosra  : SKIRRQIEECGIPYSYICCTPIAAWPYHDNTHP----------------ADVLPPLDRFQIYGDGTVK-----AY : 200
LAR1 Gosar  : RQVRRLIEKLEIPYTYICCNSIASWPYHNNTHP----------------SEVIPPLDHFEIYGDGSVK-----AY : 192
LAR1 Gosra  : RQVRRLIEKLEIPYTYICCNSIASWPYHNNRHP----------------SEVIPPLDHFEIYGDGSVK-----AY : 192
IFRL1 Vitv  : MVVRKAIEEANIPHTYVSSNCFAAYFVPNCSQLGTLT----------------PPKEKVFLYGDGNVK-----AV : 192
IFRL2 Vitv  : RIIRRAIEAAGISYTFVSANCLGAYFVNYLLHP----------------HDHSN--DSITVYGSAEAQ-----AV : 194
IFRL3 Vitv  : KKVRRATEAAGIPFTYVSANSFAAYFVDYLLHP----------------HERT---QHVSIYGNGDAK-----AV : 187
IFRL4 Vitv  : VQMRRAIEAEGIPYTFVVANCFAGYFLPTLVQ--PGVSA--------------PPRDKVIILGDGNPK-----AC : 187
IFRL5 Vitv  : AQIRRTIEAEGIPYTYVSSNFFAGYFLPSLSQ--PGATT--------------PPRDKVIILGDGNPK-----AV : 185
IFRL6 Vitv  : AQIRRTIEAEGIPYTYVSSNFFAGFFLPTLSQ--PGATA--------------PPRDKVIILGDGNPK-----AV : 187
At1g19540   : AQIRRAIEAAKIPYTYVVSGCFAGLFVPCLGQCHLRLRS--------------PPRDKVSIYDTGNGK-----AI : 189
At1g32100   : MEVRQAIEAAGIPYTYVVGACFAAYFAGNLSQMVTLL----------------PPKEKVNIYGDGNVK-----VV : 198
At1g75280   : IQIRRTIEAEGIPYTYAVTGCFGGYYLPTLVQFEPGLTS--------------PPRDKVTILGDGNAK-EYFAAV : 194
At1g75290   : LQTRRDIEAEGIPYTYLVTNYFAGYYLPTLVQLEPGLTS--------------PPRDKVKIFGDGNVKVEYFIAV : 195
At1g75300   : VQIRRAIEAEGIPYTYVVSNCSAGFYLRTLLQFESGLISHTRDKAIIFGDKNVPPRDKVTILGDGNAK-----VV : 204
At4g13660   : MEIRNAIKAAGISHTYLVGACFAAYFGGNLSQMGTLF----------------PPKNKVDIYGDGNVK-----VV : 198
At4g34540   : SEIRHMIESEGIPYTYICCGLFMRVLLPSLVQP----------------GLQSPPTDKVTVFGDGNVK-----AV : 185
At4g39230   : AKIRRTIEAEGIPYTYVSCNFFAGYFLPTLAQ--PGATS--------------APRDKVIVLGDGNPK-----AV : 187
PLR Forin   : MVVRKAIEKAGIPFTYVSANCFAGYFLGGLCQFGKIL----------------PSRDFVIIHGDGNKK-----AI : 193
PCBER Fori  : SKIRRAVEAEGIPFTFVSSNYFAGYSLPTLVQ--PGVTA--------------PPRDKVIILGDGNAK-----AV : 187
IFR Cicar   : ASIRRVVEAEGVPYTYLCCHAFTGYFLRNLAQ--FDATE--------------PPRDKVIILGDGNVK-----GA : 198
DFR At5g42  : LEFIM--SKKMTGWMYFVSKTLAEKAAWDFAEE--------------------KGLDFISIIPTLVVG-PFITTS : 201
At2g45400   : VEVFRNQKEKRVSSSYVVSKMAAETAALEFGGK--------------------NGLEVVTLVIPLVVG-PFISSS : 240
DFR Vitvi   : MEFCR--AKKMTAWMYFVSKTLAEQAAWKYAKE--------------------NNIDFITIIPTLVVG-PFIMSS : 201
DFR MAIZE   : VDFCR--RVKMTGWMYFVSKTLAEKAALAYAAE--------------------HGLDLVTIIPTLVVG-PFISAS : 206
At4g27250   : VDHVL--KTQASGWIYVLSKLVSEEEAFRYAKE--------------------RGMDLVSVITTTVSG-PFLTPF : 214
ANR Medtr   : VEFLN--TAKPPTWGYPVSKVLAEKAAWKFAEE--------------------NNIDLITVIPTLTIG-PSLTQD : 208
ANR Arath   : VEFLT--EEKPFNWGYPISKVLAEKTAWEFAKE--------------------NKINLVTVIPALIAG-NSLLSD : 207
ANR Phaco   : VEFLN--TAKPPTWGYPVSKALAEKAAWKFAEE--------------------NHIDLITVIPALTTG-PSLTPD : 205
ANR Gosar   : IEFLS--SAKPPTWGYPASKTLAEKAAWKFAEE--------------------NNIDLITVIPSLMTG-PSLTPI : 205
ANR_Vitvi   : IEFLT--SAKPPTWGYPASKTLAEKAAWKFAEE--------------------NNIDLITVIPTLMAG-SSLTSD : 206
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                      *       320         *       340         *       360         *
LAR Orysa  : FVAGSDIGKFTIRAAYDARSIN-KIVHFRPACNLLSTNEMASLWESKIGRTLP--RVTLTEEDLIAMAADDIIPE : 278
LAR Desun  : FIDGNDIGKFTMKTIDDIRTLN-KNVHFRPSSNCYSINELASLWEKKIGRTLP--RFTVTADKLLAHAAENIIPE : 268
LAR1 Pinta : FVTGDDIGAYTMKAVDDPRTLN-KSIHFRPPKNFLNLNELADIWENKINRTLP--RVSVSAEDLVMIAKANFMPS : 310
LAR1 Vitvi : FVAGTDIGKFTMKTVDDVRTLN-KSVHFRPSCNCLNINELASVWEKKIGRTLP--RVTVTEDDLLAAAGENIIPQ : 266
LAR2 Vitvi : FVAGTDIGKFTIKTINDDRTVN-KSLHFRPPSNLVSINELASLWEKKIGRTLP--RVTVEEDDLLAAAAEMCIPD : 277
LAR1 Vitsh : FVAGTDIGKFTMKTVDDVRTLN-KSVHFRPSCNCLNINELASVWEKKIGRTLP--RVTVTEDDLLAAAGENIIPQ : 266
LAR Horvu  : FVAGTDIGKFTVKAAYDARSVN-KAVHFRPACNLLSTNEMACLWESKIGRTLP--RVTLSKEELLAMAAEDIIPE : 273
LAR Medtr  : FVDGYDIGKFTMKVVDDERTIN-KSVHFRPSTNCYSMNELASLWENKIARKIP--RAIVSEDDLLGIAAENCIPE : 269
LAR Phaco  : FVDGIDIGKFTMKVIDDVKTIN-KNVHFRPSKNCYSINELASLGEMKIGRTIP--RVTISEDDLLAAAAENCIPQ : 268
LAR2 Gosar : FVAGSDIGKFTVMSIDDDRTLN-KTVHFQPPSNLLNMNEMASLWETKIGRVLP--RVTITEQDLLQRAQEMRIPQ : 272
LAR2 Gosra : FVAGSDIGKFTVMSIDDDRTLN-KTVHFQPPSNLLNMNEMASLWETKIGRVLP--RVNITEQDLLQRAQEMRIPQ : 272
LAR1 Gosar : FVAGTDIGKFTMKTVDDIRTLN-KSVHFRPACNFYNMNELAALWERKIRRTLP--RVTVTEEDLLSAAAENIIPQ : 264
LAR1 Gosra : FVAGTDIGKFTMKTVDDIRTLN-KSVHFRPACNFYNMNELAALWERKIRRTLP--RVTVTEEDLLSAAAENIIPQ : 264
IFRL1 Vitv : FVDEDDVAAYTIKAIDDPRTLN-KTVYVRPPENILSQRQIIEMWEKLTGKKLD--KSSISAEEFLVSMKGLDYAG : 264
IFRL2 Vitv : LNYEEDIALYTIKVANDPTACX-SDSHFSAPKNIISQLELIALWEKKTGRSFK--RVHVSKEELVKLSETLPNPQ : 266
IFRL3 Vitv : LNFEEDVAAYTIRASVDPKSNANRVIIYRPPGNIVSQLDLIFFWEKKTGTKLQ--RTHIPEQDIIELFESLPFPE : 260
IFRL4 Vitv : FNREDDIGTYTIKAVDDPRTLN-KILYIKPPNSTLSFNELVSLWESKIGKTLE--KVYVPEEQVLKDIQEAPMPI : 259
IFRL5 Vitv : FNKEDDIGTYTIKAVNDPRTLN-KILYIRPPQNTYSFNDLVSLWEKKIGKTLE--KIYVPEEQVLKNIQEASVPL : 257
IFRL6 Vitv : FNKEDDIGTYTIKAADDPRALN-KILYIRPPQNTYSFNEIVSLWEKKIGKTLE--KIYVPEEQVLKNIQEASFPL : 259
At1g19540  : VNTEEDIVAYTLKAVDDPRTLN-KILYIHPPNYIVSQNDMVGLWEEKIGKTLE--KTYVSEEELLKTIQESKPPM : 261
At1g32100  : FADEDDIAKYTAKTLNDPRTLN-KTVNIRPPDNVLTQLELVQIWEKLTGKELE--KTNIAAQDFLANIEQMEIPH : 270
At1g75280  : INKEEDIAAYTIKAVDDPRTLN-KILYIKPSNNTLSMNEIVTLWEKKIGKSLE--KTHLPEEQLLKSIQESPIPI : 266
At1g75290  : INKEEDIAAYTIKAVDDPRTLN-KTLYINPPNNTLSMNEIVTLWEKKIGKSVE--KIYMSEEQIFKSIQESPVPF : 267
At1g75300  : INKEEDVAAYMIKAVDDLRTLN-KTLYISPPNNILSMNEMVTLWEKKIGKSLE--KTHISEEQILKSIQ---VPI : 273
At4g13660  : FVDEDDMAKYTAKTLNDPRTLN-KTVYVRPTDNILTQMELVQIWEKLTEKELE--KTYVSGNDFLADIEDKEISH : 270
At4g34540  : FVNDVDVAAFTIKTIDDPRTLN-KTLYLSPPGNICSMNDLVELWEGKIEKKLE--KTFATENQLLKKIKETPYPD : 257
At4g39230  : FNKEEDIGTYTINAVDDPRTLN-KILYIRPPMNTYSFNDLVSLWENKIGKTLE--RIYVPEEQLLKQIIESSPPL : 259
PLR Forin  : YNNEDDIATYAIKTINDPRTLN-KTIYISPPKNILSQREVVQTWEKLIGKELQ--KITLSKEDFLASVKELEYAQ : 265
PCBER Fori : FNEEHDIGTYTIKAVDDPRTLN-KILYIKPPKNIYSFNELVALWENKIGKTLE--KIYVQEEQLIKQIEESPFPI : 259
IFR Cicar  : YVTEADVGTYTIRAANDPRTLN-KAVHIRLPHNYLTSNEVVSLWEKKIGKTLE--KSYISEEKVLKDINVSTFPH : 270
DFR At5g42 : MPPSLITALSPITRNEAHYSIIR-------QGQYVHLDDLCNAHIFLYEQAAAKGRYICSSHDATILTISKFLRP : 269
At2g45400  : LPSSVFISLAMLFGNYKEKYLFD-------TYNMVHIDDVARAMIFLLEKPVAKGRYICSSVEMKIDEVFEFLST : 308
DFR Vitvi  : MPPSLITALSPITGNEAHYSIIR-------QGQFVHLDDLCNAHIYLFENPKAEGRYICSSHDCIILDLAKMLRE : 269
DFR MAIZE  : MPPSLITALALITGNAPHYSILK-------QVQLIHLDDLCDAEIFLFENPAAAGRYVCSSHDVTIHGLAAMLRD : 274
At4g27250  : VPSSVQVLLSPITGDSKLFAILSAVNKRMGSIALVHIEDICRAHLFLMEQPKAKGQYICCVDNIDMHELMLHHFS : 289
ANR Medtr  : IPSSVAMGMSLLTGNDFLINALKGMQFLSGSISITHVEDICRAHIFVAEKESTSGRYICCAHNTSVPELAKFLSK : 283
ANR Arath  : PPSSLSLSMSFITGKEMHVTGLKEMQKLSGSISFVHVDDLARAHLFLAEKETASGRYICCAYNTSVPEIADFLIQ : 282
ANR Phaco  : IPSSVGLATSLITGNDFLINALKGMQFLSGSISITHVEDICRAHIYVAENESSSGRYIVSAHSTSVPELAKFLSK : 280
ANR Gosar  : VPSSIGLATSLISGNEFLINALKGMQMLSGSISITHVEDVCRAHVFLAEKESASGRYICSAVNTSVPELAKFLNK : 280
ANR_Vitvi  : VPSSIGLAMSLITGNEFLINGMKGMQMLSGSVSIAHVEDVCQAHIFVAEKESASGRYICCAANTSVPELAKFLSK : 281
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               380         *       400         *       420         *       440         *
LAR Orysa  : SIVASLTHDIFINGCQTHFYIDGPRDIEISSLYPDIPFRTIDECFDDYIHVLNLAEEAKEEE------------- : 340
LAR Desun  : SIVSSFTHDIFINGCQVNFSIDEHSDVEIDTLYPDEKFRSLDDCYEDFVPMVHDKIHAGKSGEIKIKDGKPLVQT : 343
LAR1 Pinta : SIVAALTHDIFINGCQFKFPIQEPHHVEACELYPDIKYTTMEDFFQGYL-------------------------- : 359
LAR1 Vitvi : SVVAAFTHDIFIKGCQVNFSIDGPEDVEVTTLYPEDSFRTVEECFGEYIVKMEE---KQPTADSAIAN------- : 331
LAR2 Vitvi : SIVASFTHDIFIKGCQVNFSLDKPTDLEATSLYPEMQFRTIDECFDEFVEKIMGGQAAAEK------EG------ : 340
LAR1 Vitsh : SVVAAFTHDIFIKGCQVNFSIDGPEDVEVTTLYPEDSFRTVEECFGEYIVKIEE---KQPTADSAIAN------- : 331
LAR Horvu  : SIVASLTHDIFINGCQTNFGIDGSRDIEISSLYPDIPFRTIDECFDDYARGLHLEEEAEESK------------- : 335
LAR Medtr  : SVVASITHDIFINGCQVNFKIDGIHDVEISTLYPGESFRSLEDCFESFVAMAADKIHKGENG------------- : 331
LAR Phaco  : SIVASFTHDIFIKGCQVNFSIDGVDDVEITTLYPDEEFRSLEDCYEDFAHMIEDNIHKGEHK------------- : 330
LAR2 Gosar : SVVAAITHDIFINGCQINFSLDKTTDVEICSLYPNTSFRTIAECFDDFAKKISDNEKAVSKPVTASNTD------ : 341
LAR2 Gosra : SVVAAITHDIFINGCQINFSLDKTTDVEVCSLYPNTSFRTIAECFDDFAKKISDNEKAVSKPVTASNTD------ : 341
LAR1 Gosar : SVVASFTHDIFIKGCQINFPIEGPNETEACSLYPNEPFRTLDDCFNDFLAKMKDENMKQSDENTKQSNE------ : 333
LAR1 Gosra : SVVASFTHDIFIKGCQINFPIEGPNETEACSLYPNEPFRTLDDCFNDFVAKMKDENMKQSDENTKQSNE------ : 333
IFRL1 Vitv : QVGVGHFYHIYYEGCLTNFEIGEEG-EEASKLYPEVDYIRMDEYLKRYL-------------------------- : 312
IFRL2 Vitv : NIPVAILHSIFIKGVVMNFEIGE-DDIEVSKLYPDINYHSID---------------------------------- : 307
IFRL3 Vitv : NIPVAILHNIFIKGDQVSFELPA-NDLEASELYPDYKYTSVDKLLDLCLVNPAKPKRAAFA------------- : 320
IFRL4 Vitv : NVFLSIQHSVFVNGDQTNFEIEPSFGVEASELYPDVKYCTVDEYLSAFV-------------------------- : 308
IFRL5 Vitv : NVILSISHSVFIKGDHTNFEIEPSFGVEATELYPDVKYTTVDEYLNQFV-------------------------- : 306
IFRL6 Vitv : NVILSISHSVFIKGDHTNFEIEPSFGVEASELYPDVKYTTVDEYLDQFV-------------------------- : 308
At1g19540  : DFLVGLIHTILVKSDFTSFTIDPSFGVEASELYPEVKYTSVDEFLNRFI-------------------------- : 310
At1g32100  : QAGIGHFYHIFYEGCLTDHEVGED--EEASSLYPDVKYKRMDDYLRMFL-------------------------- : 317
At1g75280  : NVVLSINHAVFVNGD-TNISIEPSFGVEASELYPDVKYTSVDEYLSYFA-------------------------- : 314
At1g75290  : NVLLSINHAVFVKGDQTNFTIEPSFGFEASELYPDIKYTSIDEYLSYFALGTSLNT------------------- : 323
At1g75300  : DVFKSINHAVFVKGDQTSFTIEPWFGEEASVLYPDVKYTSIDEYLSQFT-------------------------- : 322
At4g13660  : QAGLGHFYHIYYEGCLTDHEVGDD--EEATKLYPDVKYKRMDEYLKIFV-------------------------- : 317
At4g34540  : NMEMVFIYSVFIKGDHTYFDIESCGGVNGTELYPDVKYMTVSEFLDTLL-------------------------- : 306
At4g39230  : NVMLSLCHCVFVKGGHTSFEIEPSFGVEASELYPDVKYTTVDEILNQYV-------------------------- : 308
PLR Forin  : QVGLSHYHDVNYQGCLTSFEIGDE--EEASKLYPEVKYTSVEEYLKRYV-------------------------- : 312
PCBER Fori : NIVLAINHSVFVKGDLTNFKIEPSFGVEASELYPDVKYTTVEEYLSHFV-------------------------- : 308
IFR Cicar  : NYLLALYHSQQIKGD-AVYEIDPAKDAEAYDLYPDVKYTTADEYLDQFV-------------------------- : 318
DFR At5g42 : KYPEYNVPSTFEGVDE-NLKSIEFSSKKLTDMGFNFKYS-LEEMFIESIETCRQKGFLPVSLSYQSISEIKTKNE : 342
At2g45400  : KFPQFQLPSIDLNKYK-VEKRMGLSSKKLKSAGFEFKYG-AEEIFSGAIRSCQARGFL----------------- : 364
DFR Vitvi  : KYPEYNIPTEFKGVDE-NLKSVCFSSKKLTDLGFEFKYS-LEDMFTGAVDTCRAKGLLRP-----------SHEK : 331
DFR MAIZE  : RYPEYDVPQRFPGIQD-DLQPVRFSSKKLQDLGFTFRYKTLEDMFDAAIRTCQEKGLIPL-----------ATAA : 337
At4g27250  : KDYLCKVQKVNEDEEERECMKPIISSKKLRELGFEYKYG-IEEIVDQTIDASIKIKFPTLNHKLRQ--------- : 354
ANR Medtr  : RYPQYKVPTEFDDFPS-KAK-LIISSGKLIKEGFSFKHS-IAETFDQTVEYLKTQG-IK---------------- : 338
ANR Arath  : RYPKYNVLSEFEEGLS-IPK-LTLSSQKLINEGFRFEYG-INEMYDQMIEYFESKGLIKAK-------------- : 340
ANR Phaco  : RYPQYKVPTEFDDCPS-KAK-LTISSEKLVKEGFSFKYG-IEEIYDQTVEYLKNKGTLKN--------------- : 337
ANR Gosar  : RYPDFKVPTDFGDFPS-KPK-LIISSEKLISEGFSFKYG-IEEIYDQTVEYLKSKGLLK---------------- : 336
ANR_Vitvi  : RYPQYKVPTDFGDFPP-KSK-LIISSEKLVKEGFSFKYG-IEEIYDESVEYFKAKGLLQN--------------- : 338
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                    460         *       480         *       500         *       520
LAR Orysa  : -----------------------KKNAPTVGRLAIPPTCA----------------------------------- : 357
LAR Desun  : GTIEEINKDIKTLVETQPNEEIKKDMKALVEAVPISAMG------------------------------------ : 382
LAR1 Pinta : --------------------------------------------------------------------------- :   -
LAR1 Vitvi : -------------------------TGPVVGMRQVTATCA----------------------------------- : 346
LAR2 Vitvi : ----------------------IVVPASAPDALVITATCA----------------------------------- : 358
LAR1 Vitsh : -------------------------TGPVVGMRQVTATCA----------------------------------- : 346
LAR Horvu  : -----------------------KSNAPMVEILAVYPTCA----------------------------------- : 352
LAR Medtr  : ---------------------VTGGTKALVEPVPITASC------------------------------------ : 349
LAR Phaco  : ---------------------ITG-TKSVVEAVPIMASCGNIYE------------------------------- : 352
LAR2 Gosar : ----------------------IFVPTAKPEALAITAICT----------------------------------- : 359
LAR2 Gosra : ----------------------IFVPTAKPEALAITAICT----------------------------------- : 359
LAR1 Gosar : ----------------------IPPPKPVVEAFAITATCALTLKISTPNYPFSLLHSCRDIKSISMGVITFLFPL : 386
LAR1 Gosra : ----------------------IPPPKPVVEAFAITATCA----------------------------------- : 351
IFRL1 Vitv : --------------------------------------------------------------------------- :   -
IFRL2 Vitv : --------------------------------------------------------------------------- :   -
IFRL3 Vitv : --------------------------------------------------------------------------- :   -
IFRL4 Vitv : --------------------------------------------------------------------------- :   -
IFRL5 Vitv : --------------------------------------------------------------------------- :   -
IFRL6 Vitv : --------------------------------------------------------------------------- :   -
At1g19540  : --------------------------------------------------------------------------- :   -
At1g32100  : --------------------------------------------------------------------------- :   -
At1g75280  : --------------------------------------------------------------------------- :   -
At1g75290  : --------------------------------------------------------------------------- :   -
At1g75300  : --------------------------------------------------------------------------- :   -
At4g13660  : --------------------------------------------------------------------------- :   -
At4g34540  : --------------------------------------------------------------------------- :   -
At4g39230  : --------------------------------------------------------------------------- :   -
PLR Forin  : --------------------------------------------------------------------------- :   -
PCBER Fori : --------------------------------------------------------------------------- :   -
IFR Cicar  : --------------------------------------------------------------------------- :   -
DFR At5g42 : NIDVKTGDGLTDGMKPCNKTETGITGERTDAPMLAQQMCA----------------------------------- : 382
At2g45400  : --------------------------------------------------------------------------- :   -
DFR Vitvi  : PVDGKT--------------------------------------------------------------------- : 337
DFR MAIZE  : GGDGFAS------VRAPGETEATIGA------------------------------------------------- : 357
At4g27250  : --------------------------------------------------------------------------- :   -
ANR Medtr  : --------------------------------------------------------------------------- :   -
ANR Arath  : --------------------------------------------------------------------------- :   -
ANR Phaco  : --------------------------------------------------------------------------- :   -
ANR Gosar  : --------------------------------------------------------------------------- :   -
ANR_Vitvi  : --------------------------------------------------------------------------- :   -
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                 *
LAR Orysa  : --------- :   -
LAR Desun  : --------- :   -
LAR1 Pinta : --------- :   -
LAR1 Vitvi : --------- :   -
LAR2 Vitvi : --------- :   -
LAR1 Vitsh : --------- :   -
LAR Horvu  : --------- :   -
LAR Medtr  : --------- :   -
LAR Phaco  : --------- :   -
LAR2 Gosar : --------- :   -
LAR2 Gosra : --------- :   -
LAR1 Gosar : LILWEGNWI : 395
LAR1 Gosra : --------- :   -
IFRL1 Vitv : --------- :   -
IFRL2 Vitv : --------- :   -
IFRL3 Vitv : --------- :   -
IFRL4 Vitv : --------- :   -
IFRL5 Vitv : --------- :   -
IFRL6 Vitv : --------- :   -
At1g19540  : --------- :   -
At1g32100  : --------- :   -
At1g75280  : --------- :   -
At1g75290  : --------- :   -
At1g75300  : --------- :   -
At4g13660  : --------- :   -
At4g34540  : --------- :   -
At4g39230  : --------- :   -
PLR Forin  : --------- :   -
PCBER Fori : --------- :   -
IFR Cicar  : --------- :   -
DFR At5g42 : --------- :   -
At2g45400  : --------- :   -
DFR Vitvi  : --------- :   -
DFR MAIZE  : --------- :   -
At4g27250  : --------- :   -
ANR Medtr  : --------- :   -
ANR Arath  : --------- :   -
ANR Phaco  : --------- :   -
ANR Gosar  : --------- :   -
ANR_Vitvi  : --------- :   -
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